

Resource Summary Report

Generated by [dkNET](#) on Aug 16, 2026

RCircos

RRID:SCR_003310

Type: Tool

Proper Citation

RCircos (RRID:SCR_003310)

Resource Information

URL: <http://cran.r-project.org/web/packages/RCircos/>

Proper Citation: RCircos (RRID:SCR_003310)

Description: Software package that provides a simple and flexible way to generate Circos 2D track plot images for genomic data visualization. The types of plots include: heatmap, histogram, lines, scatterplot, tiles and plot items for further decorations include connector, link (lines and ribbons), and text (gene) label. All functions require only R graphics package that comes with R base installation.

Synonyms: RCircos: Circos 2D Track Plot

Resource Type: software resource

Defining Citation: [PMID:23937229](#)

Keywords: standalone software, unix/linux, mac os x, windows, r

Availability: Free, Available for download, Freely available

Resource Name: RCircos

Resource ID: SCR_003310

Alternate IDs: OMICS_04661

Alternate URLs: <https://bitbucket.org/henryhzhang/rcircos/>

Record Creation Time: 20220129T080218+0000

Record Last Update: 20260815T182231+0000

Ratings and Alerts

No rating or validation information has been found for RCircos.

No alerts have been found for RCircos.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 285 mentions in open access literature.

Listed below are recent publications. The full list is available at [dkNET](#) .

Liu X, et al. (2026) Cancer-associated fibroblasts and immune escape-related genes serve as biological markers for the prognosis of colorectal cancer. *Hereditas*, 163(1).

Li S, et al. (2026) Utilizing bulk and single-cell RNA sequencing to identify potential biomarkers linked to angiogenesis and integrated stress response in chondrosarcoma. *Scientific reports*, 16(1).

Kou R, et al. (2026) Unveiling prognostic genes and regulatory mechanisms of stress granules in gastric cancers: an integrated analysis of bulk transcriptomics and single-cell RNA sequencing. *Frontiers in oncology*, 16, 1750088.

Zhao X, et al. (2026) Identification and validation of mitochondrial metabolism-related biomarkers in coronary heart disease. *Medicine*, 105(7), e47595.

Ma T, et al. (2026) Identification and validation of biomarkers of Shenggu Zaizao Wan in the treatment of steroid-induced osteonecrosis of the femoral head by integrating network pharmacology and bulk transcriptomic. *Frontiers in medicine*, 13, 1732825.

Wen Y, et al. (2026) Integrative multi-omics reveals that downregulation of HLA-DPA1/DPB1 drives macrophage immune-metabolic dysregulation in pediatric asthma. *Frontiers in immunology*, 17, 1835475.

Pradhan B, et al. (2026) Dynamic and Ongoing De Novo L1 Retrotransposition Contributes to Genome Plasticity and Intrapatient Heterogeneity in Ovarian Cancer. *Cancer research*, 86(4), 1073.

Ling S, et al. (2026) Integrative omics and experimental validation reveal METTL17 and SLC27A1 as biomarkers and potential therapeutic targets in chronic kidney disease. *Frontiers in immunology*, 17, 1724740.

Xia Y, et al. (2026) Identification of biomarkers associated with endoplasmic reticulum stress-related cell death in osteoporosis based on bulk and single-cell transcriptomic analyses and experimental validation. *Scientific reports*, 16(1).

Luo J, et al. (2026) Identification of biomarkers related to γ -aminobutyric acid-associated genes in membranous nephropathy based on transcriptome data and clinical experiments.

Hereditas, 163(1).

Du Y, et al. (2026) IL6/IL10/TLR4 Govern Immunogenic Cell Death in Aortic Dissection. Cardiovascular therapeutics, 2026(1), e4140685.

Jin Y, et al. (2026) m6A target gene signatures reveal immune-related diagnostic biomarkers in systemic sclerosis-associated pulmonary arterial hypertension. Journal of thoracic disease, 18(5), 504.

Jiang F, et al. (2026) Machine learning identifies a NETs-related four-gene diagnostic signature for abdominal aortic aneurysm. Medicine, 105(21), e48987.

Zhao T, et al. (2026) Identification of key macrophage-related genes in systemic sclerosis-associated interstitial lung disease based on single-cell and bulk transcriptomic data. PloS one, 21(3), e0344166.

Weng X, et al. (2026) Identification of COL5A1 and TGFBI as key basement membrane genes and their molecular mechanisms in gestational diabetes mellitus. Medicine, 105(18), e48610.

Luo T, et al. (2026) Integrative multi-omics and network analysis identify potential targets of Chaihu Shugan Xiaozheng Formula in breast cancer. Translational oncology, 70, 102829.

Peng S, et al. (2026) Discovery of circadian rhythm-related hub genes in acute myocardial infarction: A two-sample Mendelian randomization study. Medicine, 105(3), e47228.

Lang Y, et al. (2026) The value of immunogenic cell death-related gene model in the prognosis of gastric cancer. Discover oncology, 17(1).

Jiang W, et al. (2026) Identification of core cytotoxic T lymphocyte-related subtypes, establishment of a prognostic model, and analysis tumor microenvironment infiltration in HNSC. Scientific reports, 16(1).

Zhang J, et al. (2026) The signature of pyroptosis-related gene diagnosis and immune microenvironment in preeclampsia. BMC pregnancy and childbirth, 26(1).